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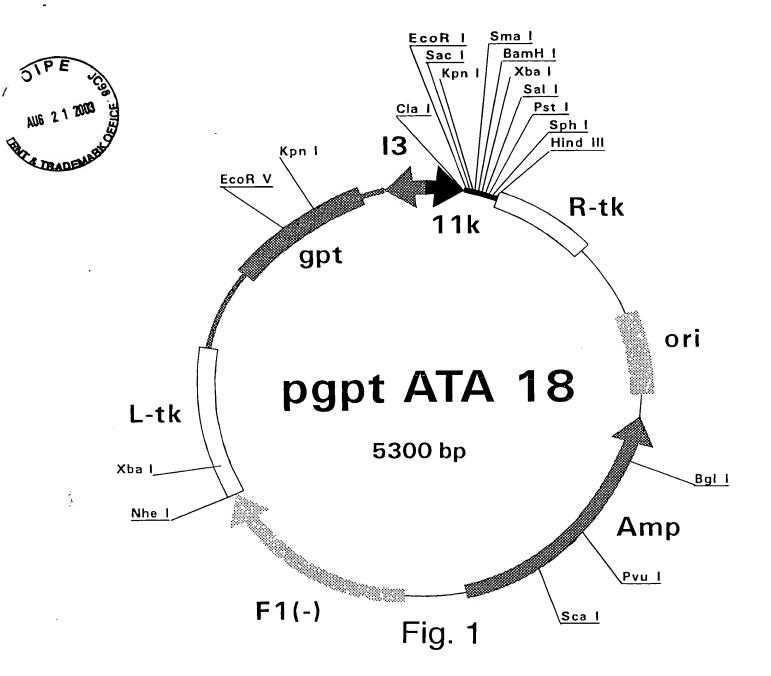
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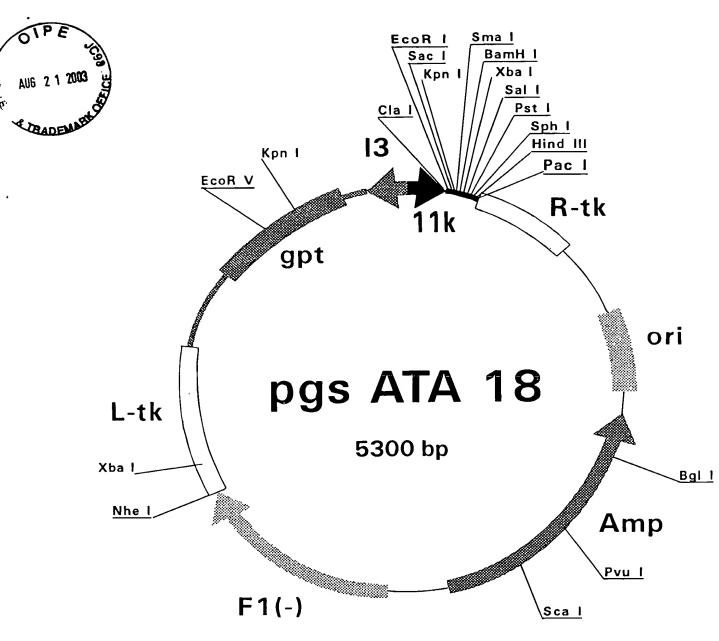


Fig. 2

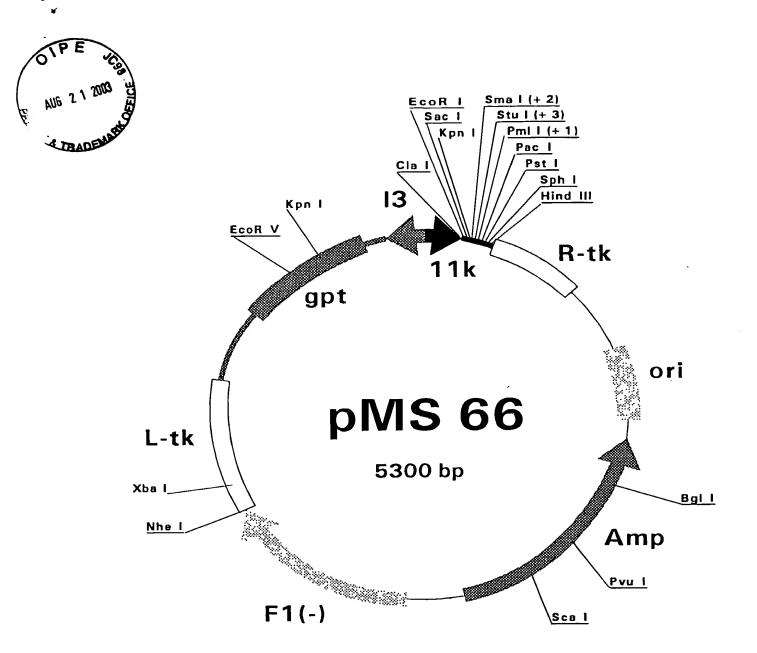


Fig. 3

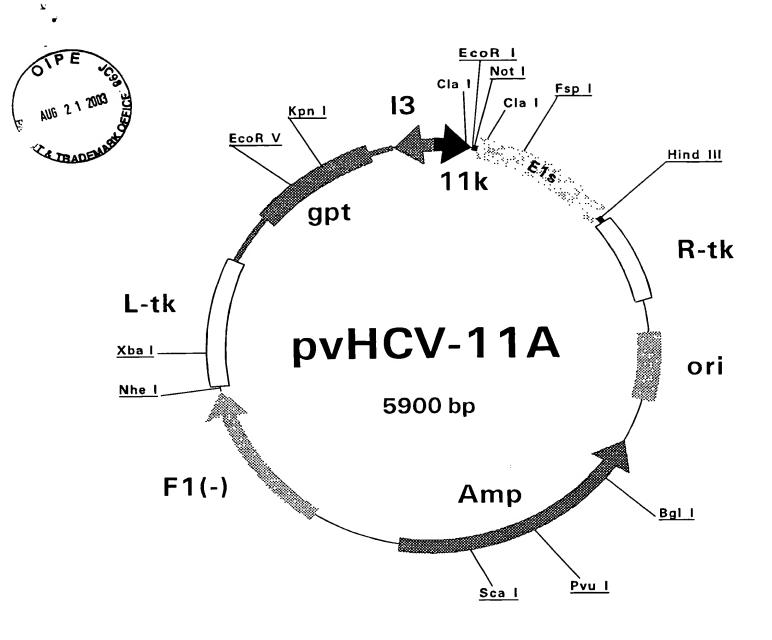
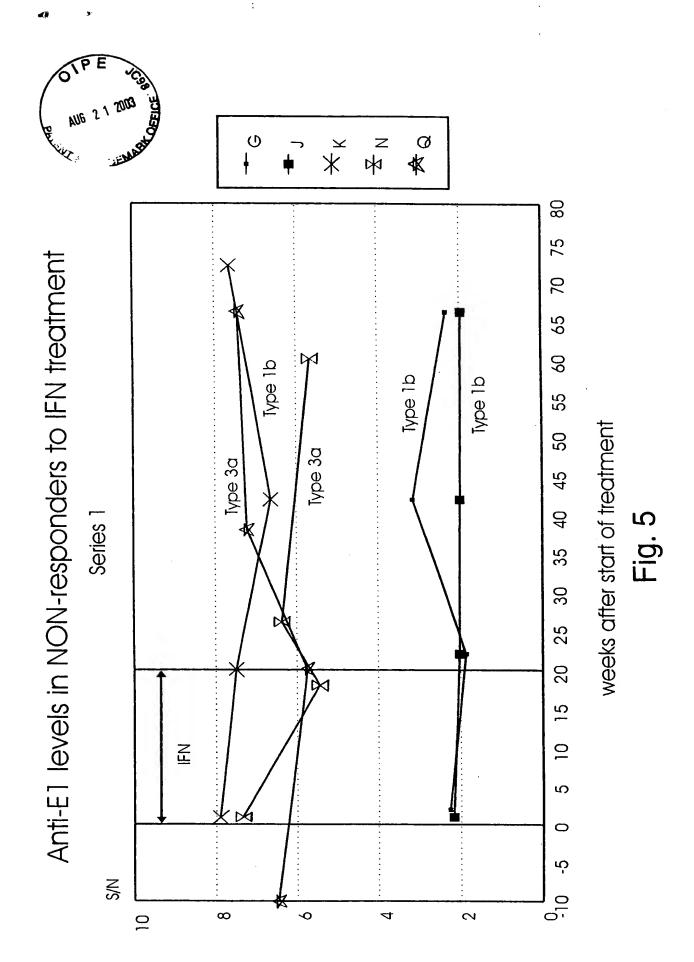
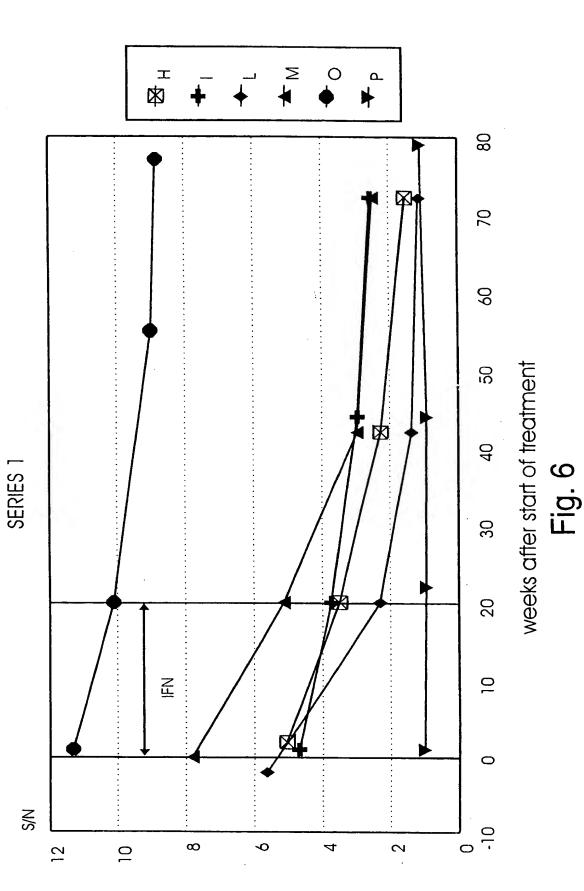


Fig. 4

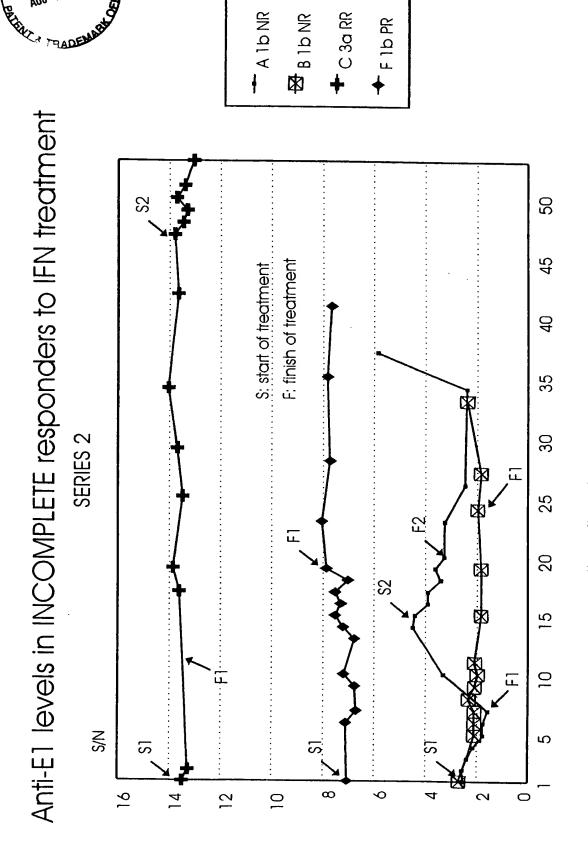




Anti-E1 levels in RESPONDERS to IFN treatment



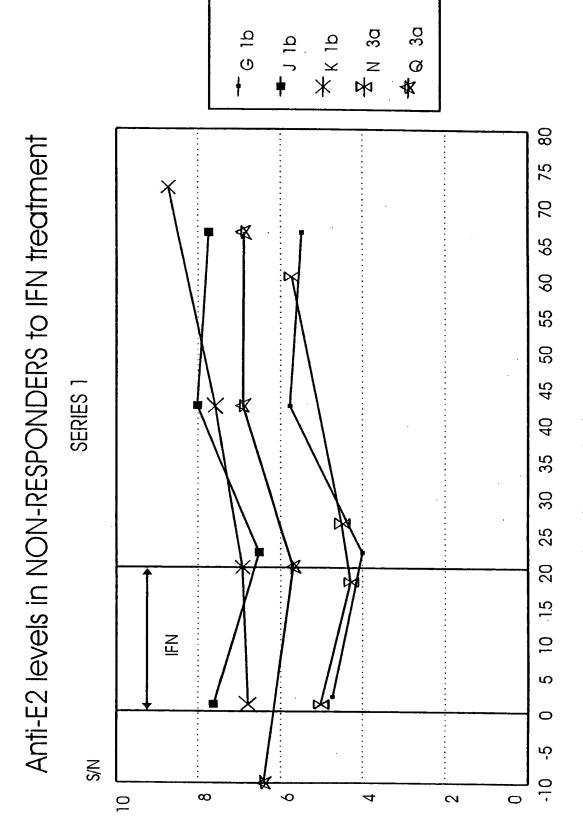
AU6 2 1 2003 **→** D 3a E 3a Anti-E1 levels in patients with COMPLETE response to IFN 20 45 49 months after start of treatment 35 30 SERIES 2 Fig. 7 25 20 15 9 S Z/S Q 2 7 ~ \bigcirc



A 1b NR

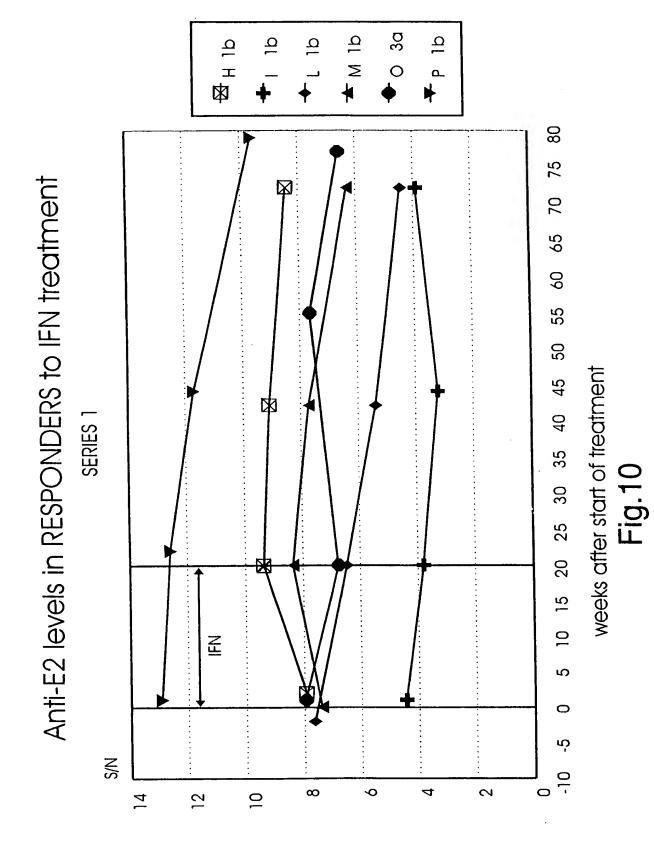
months after start of treatment Fig. 8

AUG 2 1 2003 SE

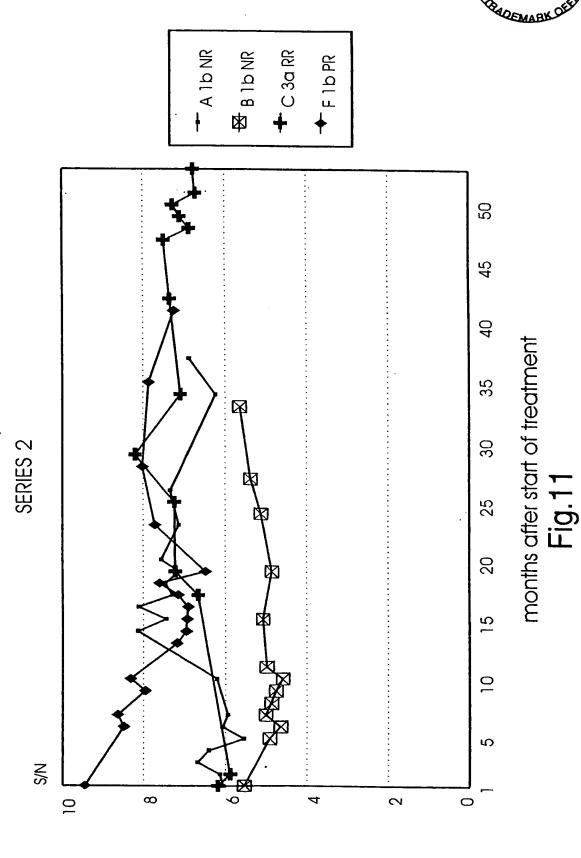


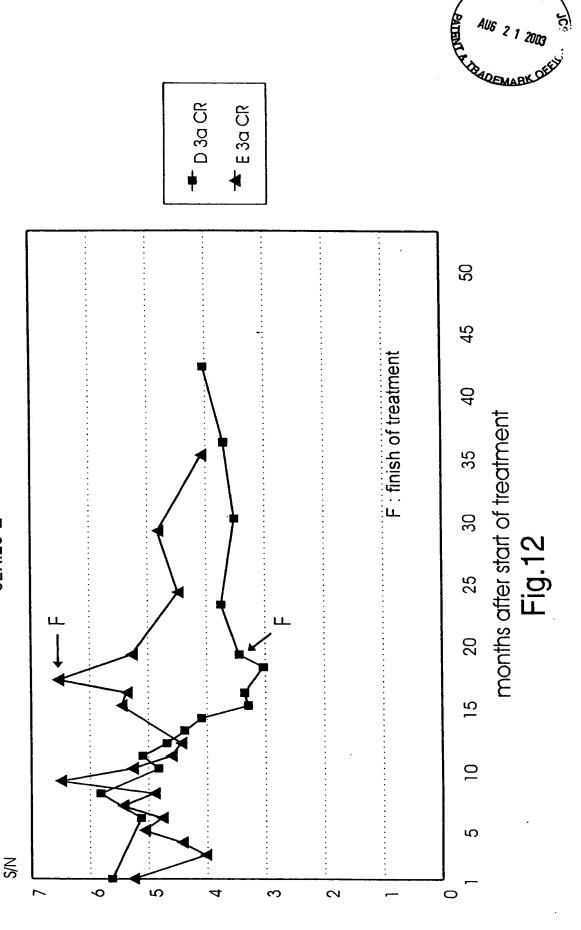
weeks after start of treatment Fig. 9





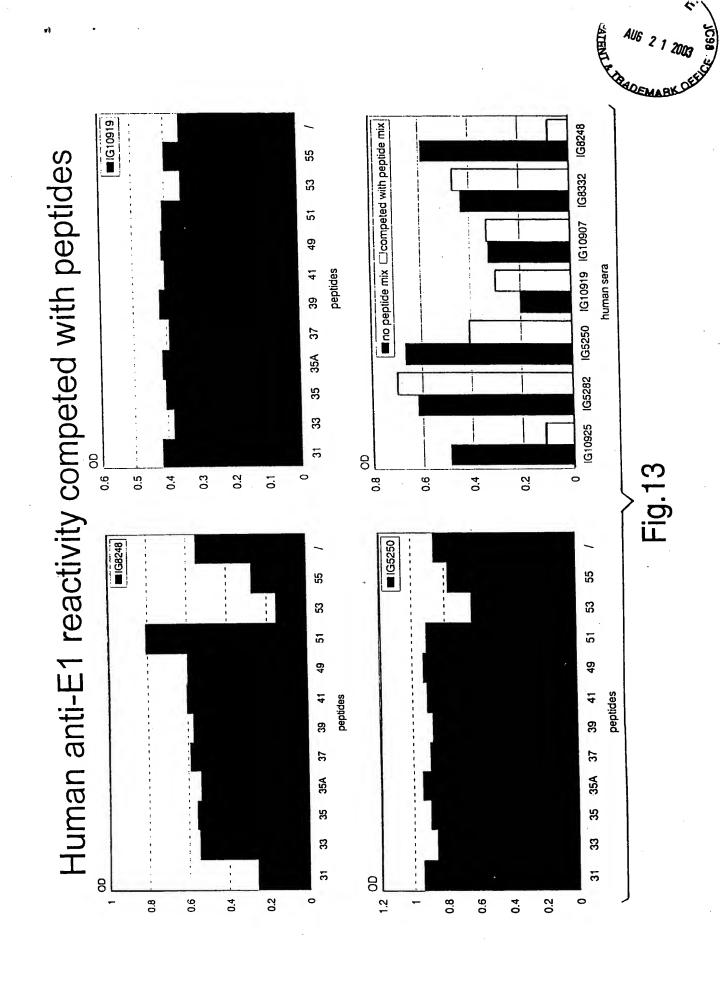
Anti-E2 levels in INCOMPLETE responders to IFN treatment

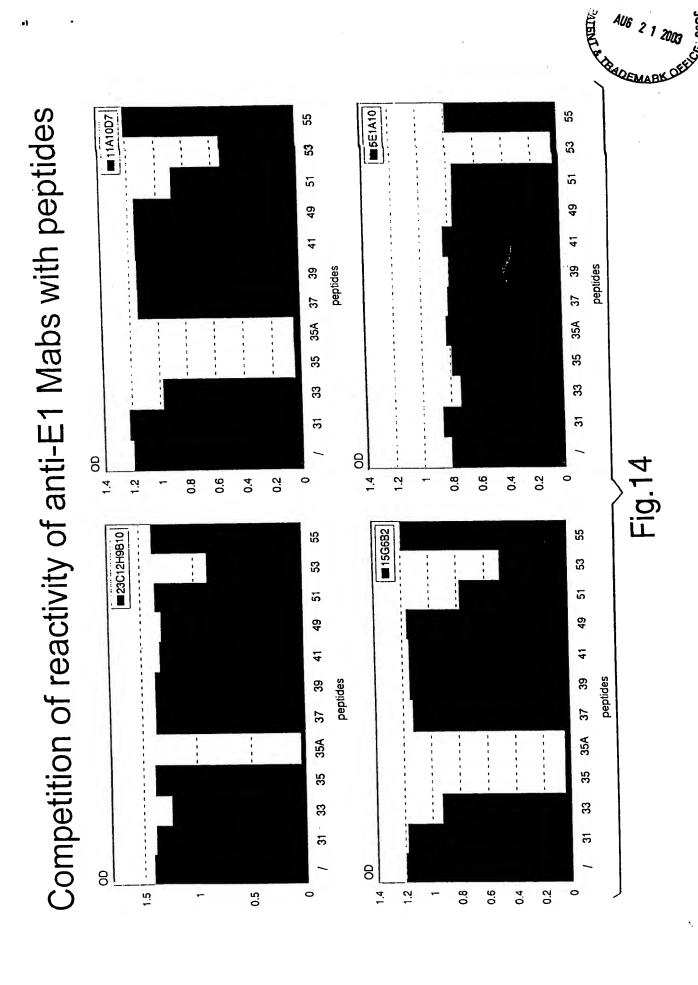




Anti-E2 levels in COMPLETE responders to IFN treatment

SERIES 2





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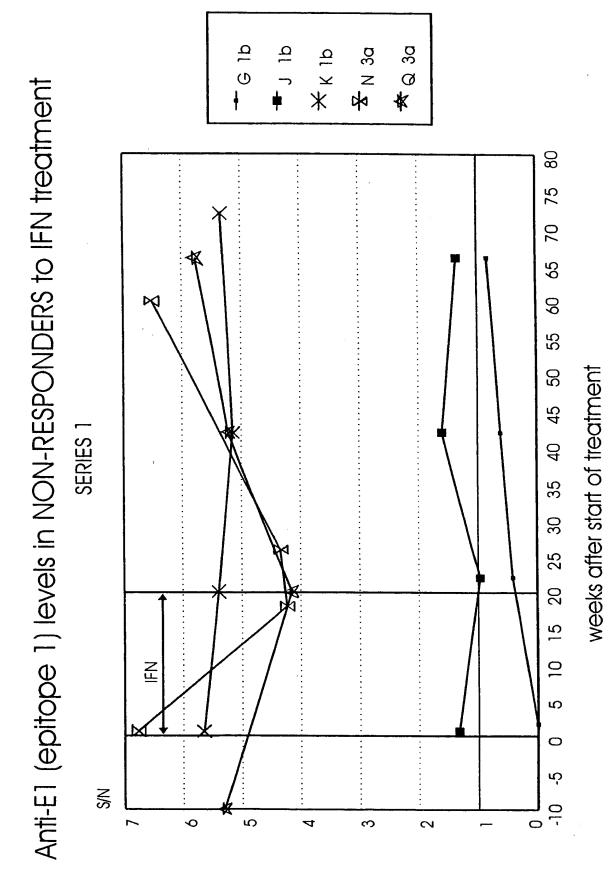
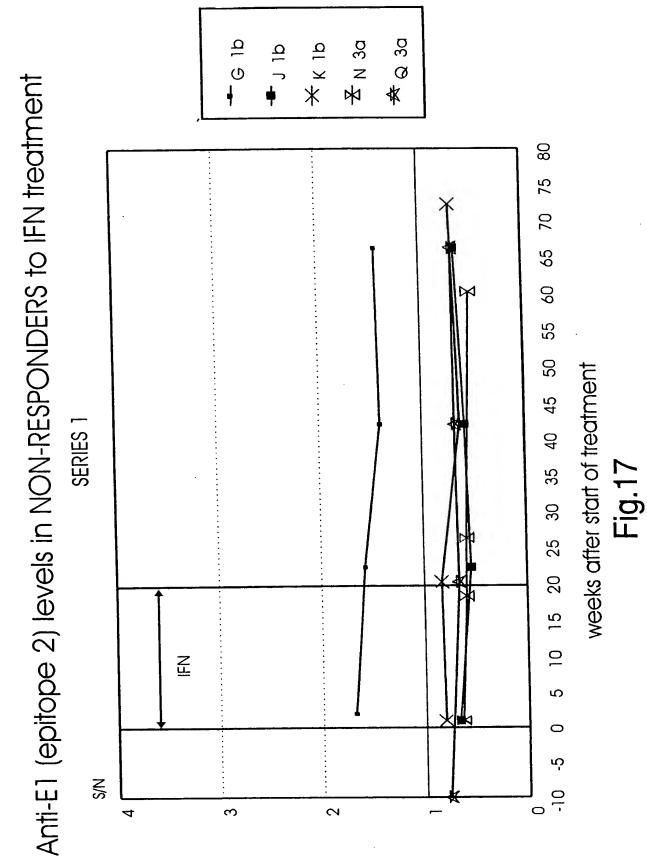


Fig.15

本 日 日 **♦** 0 3a ₩ NB + L 1b Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 weeks after start of treatment Fig.16 SERIES 1 <u>K</u> ι'n N/S ω 2 Q N 0

AUG 2 1 2000



AUG 21 2000

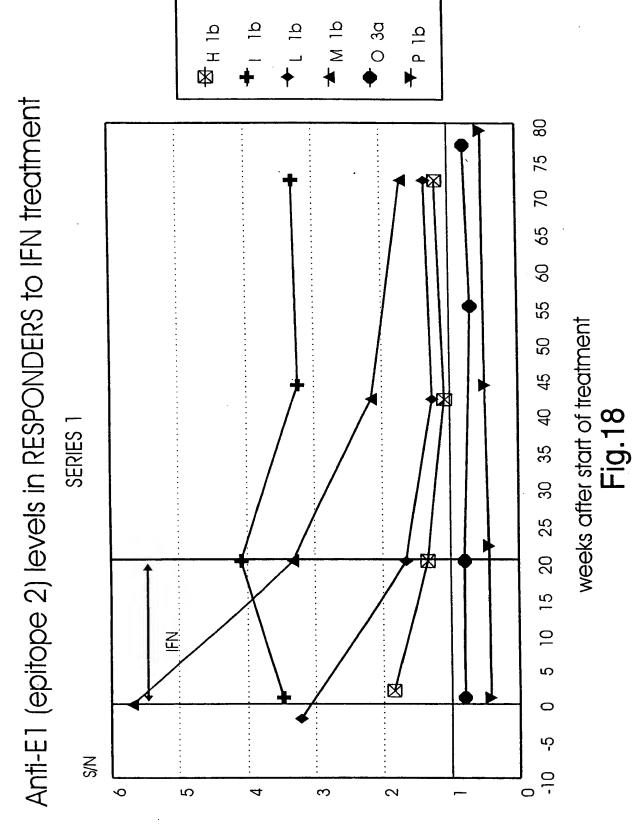




Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

SEQ ID NO 3 (HCCI9A)

SEQ ID NO 5 (HCCI10A)



Fig. 21B

SEQ ID NO 7 (HCCI11A)

SEQ ID NO 9 (HCCI12A)

SEQ ID NO 11 (HCCI13A)



Fig. 21C

GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTT
CCTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

SEQ ID NO 15 (HCPr51)
ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPr52)
ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPr53)
CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)
ATACGACGCCACGTCGATTCCCAGCTGTTCACCATC



Fig. 21D

SEQ ID NO 20 (HCPr108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

SEQ ID NO 23 (HCCI38)

SEQ ID NO 25 (HCC139)

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT



Fig. 21E

ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTCTAATAG

SEQ ID NO 27 (HCCI40)

SEQ ID NO 29 (HCCI62)

ATGGTAAGGTCATCGATACCCTTACGTGCGGATTCGCCGATCTCATGGGGTACATCC
CGCTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAATTTCGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGATATGATGATGAACTGGTAATAG



Fig. 21F

SEQ ID NO 31 (HCCl63)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACCGCTTGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCPr109)
TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCPr72)
CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)



Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCCTTCACCACCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCACCACCACCACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCCTGTTGCTCTTCCTT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCC
TGGTGCGGCATACGCCTTCTATGGCGTGGCCGCTGCTCCTTCTTCTTGCTTACCCTTAC
CACCACGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT TTGCCGGCGTCGACGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCATCGACAAGTTCGCTCAGGGGTTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGGGGGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG

SEQ ID NO 39 (HCCI42)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGGCCCCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT



Fig. 21H

TTGCCGGCGTCGACGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA CGACTCGGATGTGCTGATTCTCAACACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 41 (HCCl43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGĆTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACACGCGCGCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG CAGAGCTTAATTAATTAG



Fig. 21I

SEQ ID NO 43 (HCCI44)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCCAGCCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGGTGAT CGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 45 (HCCL64)



Fig. 21J

SEQ ID NO 47 (HCCI65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTG TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG CCACATAACGGGTCACCGTATGGCTTGGGATATGATGAACTGGTCGCCTACAACG GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG GGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGC TAAGGTTTTGGTTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTCAG GAGGGCAGCAGCCTCCGATACCAGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGC TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT GAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCG CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGGACGACCGATCGGTTTGGTGT CCCCACGTATAACTGGGGGGGGGAACGACTCGGATGTGCTGATTCTCAACACACGCGG CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCACCAAGA CGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGACCTGCC



Fig. 21K

SEQ ID NO 49 (HCCl66)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCA CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGC GCAGGGCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG CTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG GCTCCTGTCACCCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG GGTACATTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG CGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCT TTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAA GTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTG GAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCC AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTG TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC CCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTAC AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG GCGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACT GGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGT GTCAGGAGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGG



Fig. 21L

TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT GCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC ACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAA GTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC ACGCGGCCGCCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCA CCAAGACGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGA CCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC ACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA GGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC CTGTTCCTTCACCACCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCATCA AATGGGAGTATGTCCTGTTGCTCTTCCTTCCTGGCAGACGCGCGCATCTGCGCCTGC TTATGGATGATGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCC TCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTGTTCTTCTGT GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTATGGCG TGTGGCCGCTGCTCCTGCTTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA



Fig. 22

OD measured at 450 nm construct

Fraction	volume o	dilution	39 Type Ib	40 Type 1b	62 Type 3a	63 Type 5a
START FLOW THROU 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	JGH 23 i	1/20 ml 1/20 1/200	2.517 0.087 0.102 0.396 2.627 3 2.694 2.408 2.176 1.461 1.286 0.981 0.812 0.373 0.653 0.441 0.321	1.954 0.085 0.051 0.550 2.603 2.967 2.810 2.499 2.481 1.970 1.422 0.926 0.781 0.650 0.432 0.371 0.348 0.374	1.426 0.176 0.048 0.090 2.481 3 2.640 1.359 0.347 1.624 0.887 0.543 0.294 0.294 0.239 0.145 0.151 0.098	1.142 0.120 0.050 0.067 2.372 2.694 2.154 1.561 1.390 0.865 0.604 0.519 0.294 0.199 0.209 0.184 0.151 0.106
17 18 19			0.525 0.351 0.192	0.186 0.171 0.164	0.099 0.083 0.084	0.108 0.090 0.087

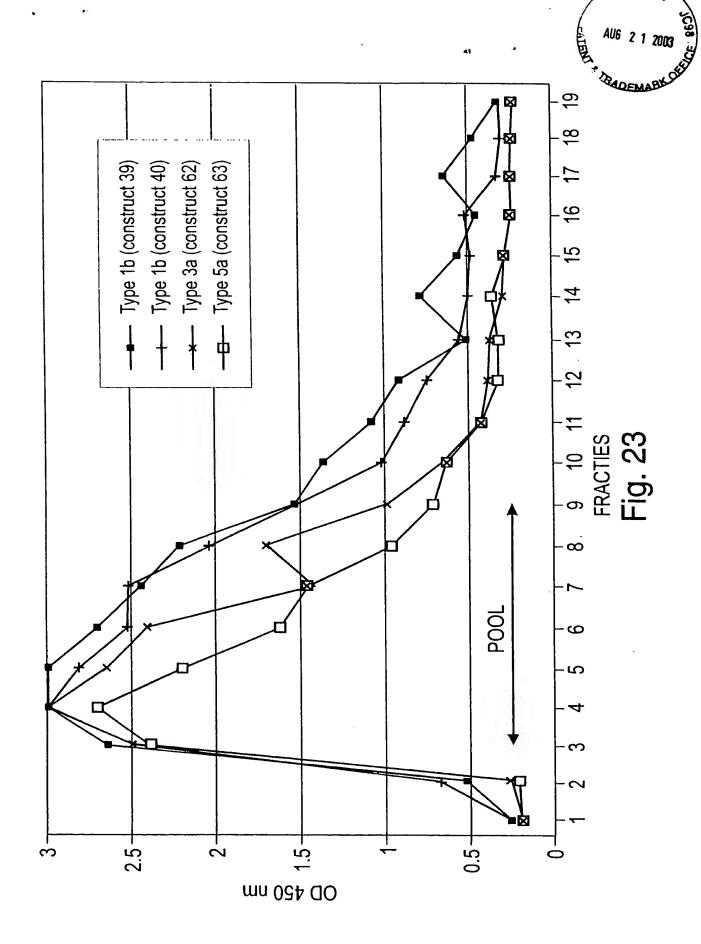




Fig. 24

OD measured at 450 nm

	construct								
Fraction	volunie	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a			
20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38	250 μl	1/200	0.072 0 109 0 279 0.093 0 080 0.251 3 3 3 2 227 0 263 0.071 0.103 0 045 0.045 0.045 0.045 0.045	0 130 0 293 0 249 0.151 0.266 0 100 1 649 3 3 3 1.921 0.415 0.172 0.054 0.045 0.045 0.047 0.045	0.096 0.084 0.172 0.297 0.438 0.457 0.722 2.528 3 2.849 1.424 0.356 0.154 0.096 0.044 0.045 0.045 0.049 0.046 0.047	0.051 0.052 0.052 0.054 0.056 0.048 0.066 0.889 2.345 2.580 1.333 0.162 0.064 0.057 0.051 0.046 0.040 0.048 0.057			
39 40			0.045 0.046	0.048 0.049	0 050 0.048	0 057 0 049			



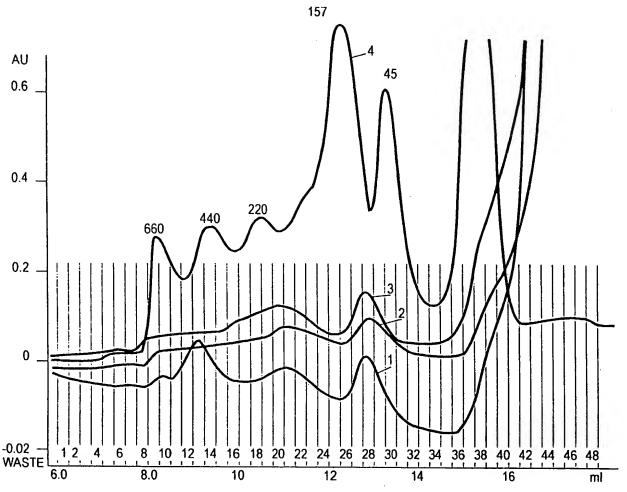


Fig. 25



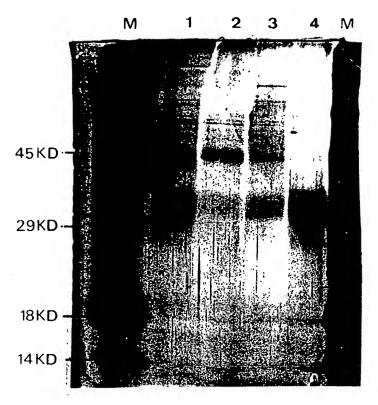


Fig. 26

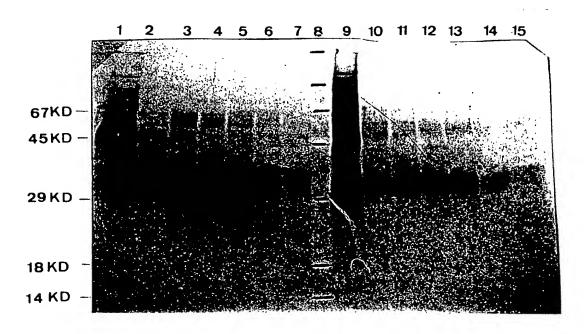


Fig.27



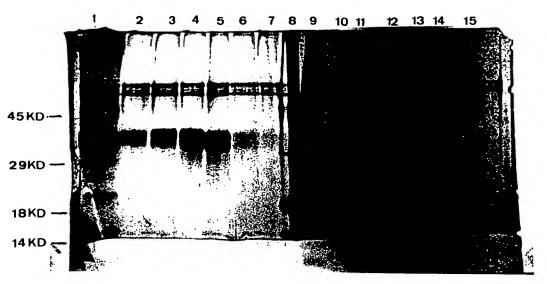


Fig.28

M 1 2 3 4 5 6 Fig. 29

67 kD
45 kD
29 kD -

18 kD -

14 kD -

Lane 1: Crude Lysate

Lane 2: Flow through Lentil Chromatography

Lane 3: Wash with EMPIGEN Lentil Chromatography

Lane 4: Eluate Lentil Chromatography

Lane 5: Flow through during concentration lentil eluate

Lane 6: Pool of Elafter Size Exclusion Chromatography



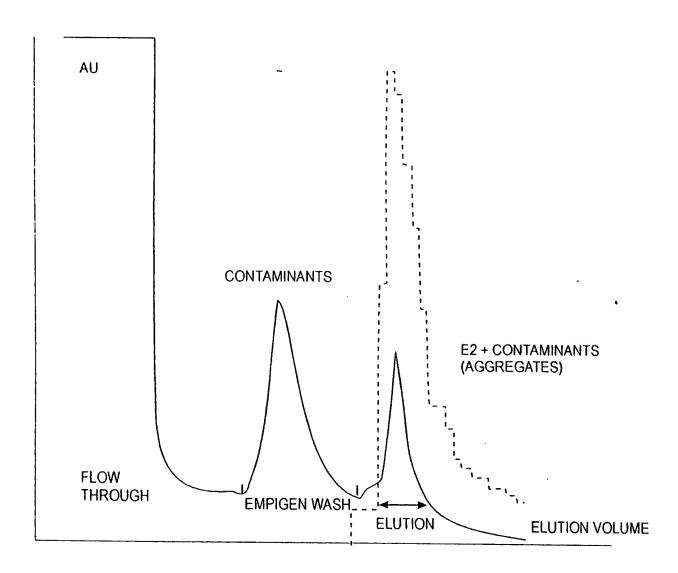
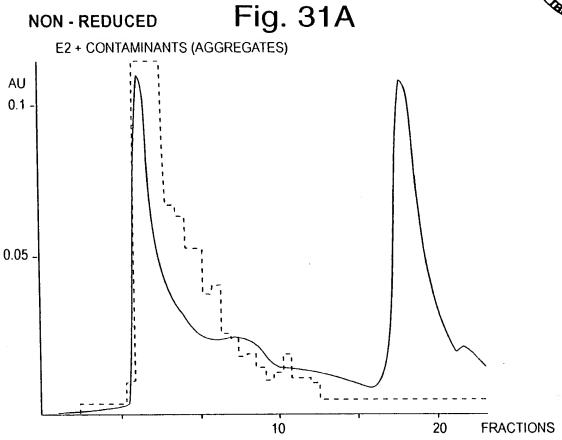


Fig. 30





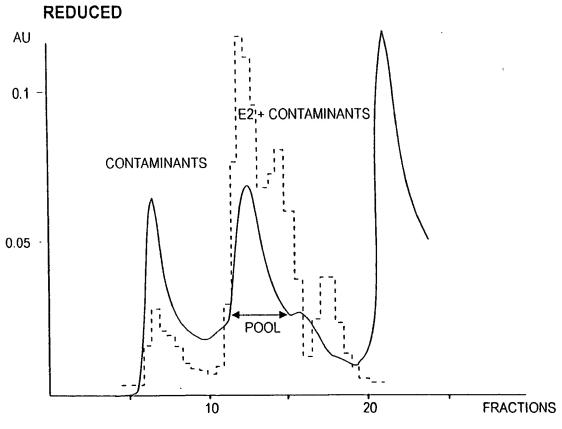
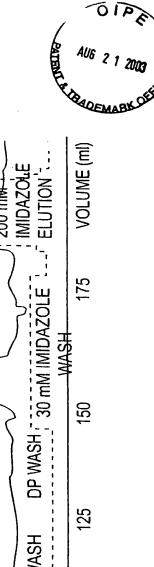


Fig. 31B



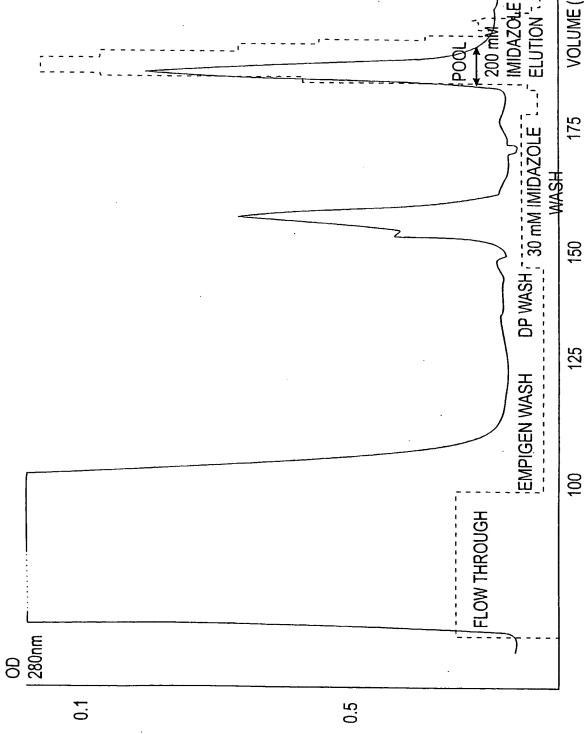
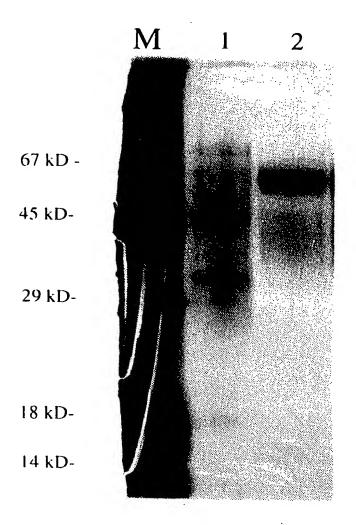


Fig. 32



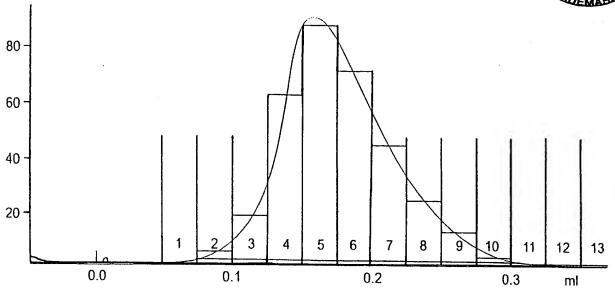
SILVER STAIN OF PURIFIED E2



30 mM IMIDAZOLE WASH Ni-IMAC
 0.5 ug E2

Fig.33

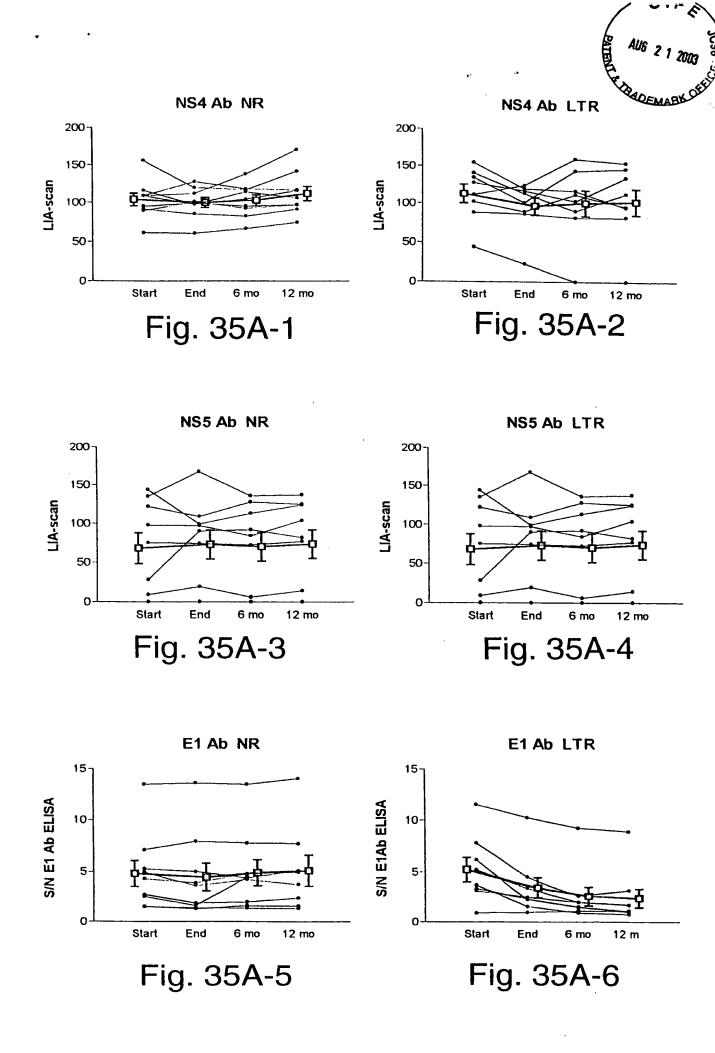




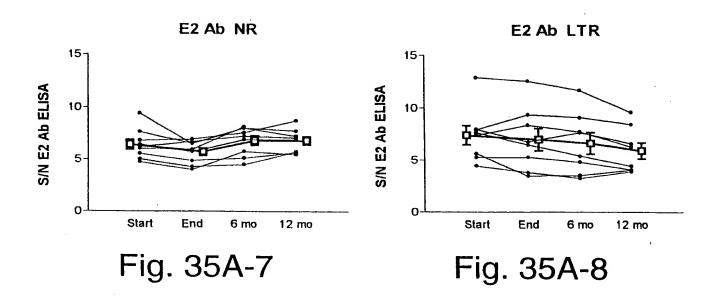
No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4,579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
Total Area above baseline = 0.796522 ml*AU
Total area in evaluated peaks = 0.796521 ml*AU
Ratio peak area / total area = 0.999999
Total peak duration = 2.613583 ml

Fig. 34









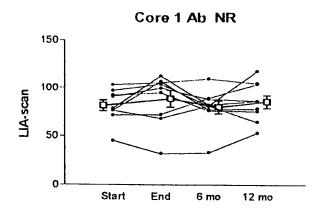


Fig. 35B-1

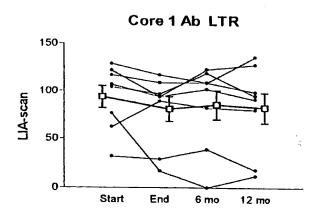


Fig. 35B-2

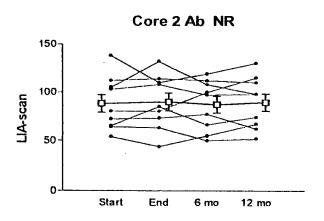


Fig. 35B-3

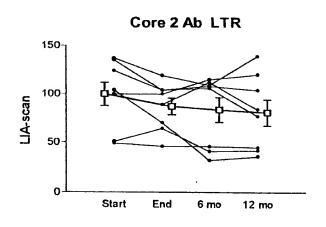


Fig. 35B-4

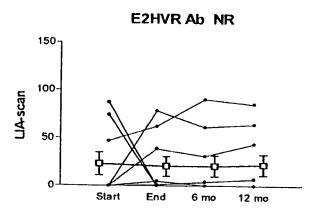


Fig. 35B-5

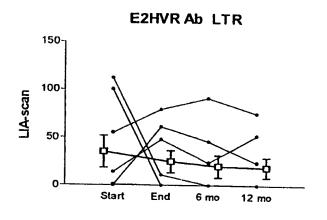


Fig. 35B-6



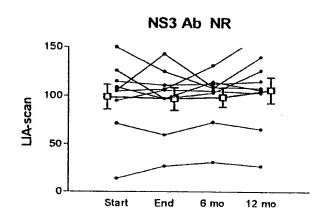


Fig. 35B-7

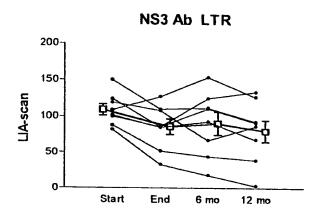


Fig. 35B-8



Fig. 36A **E1 Ab**

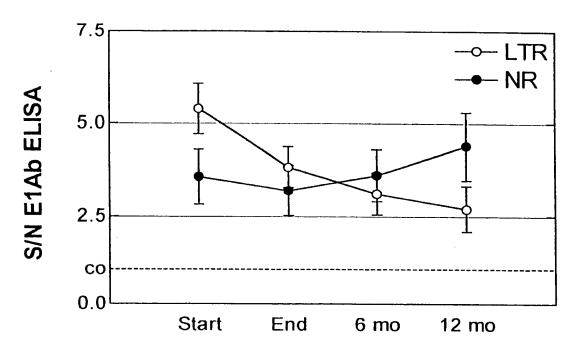
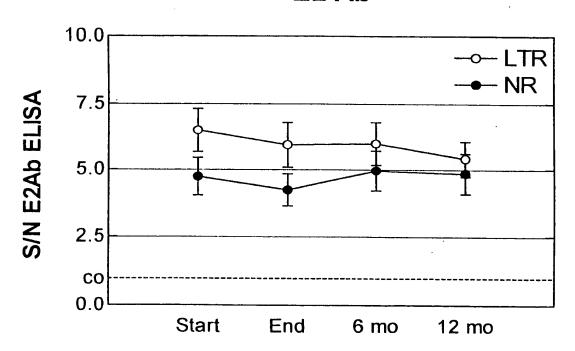


Fig. 36B **E2 Ab**



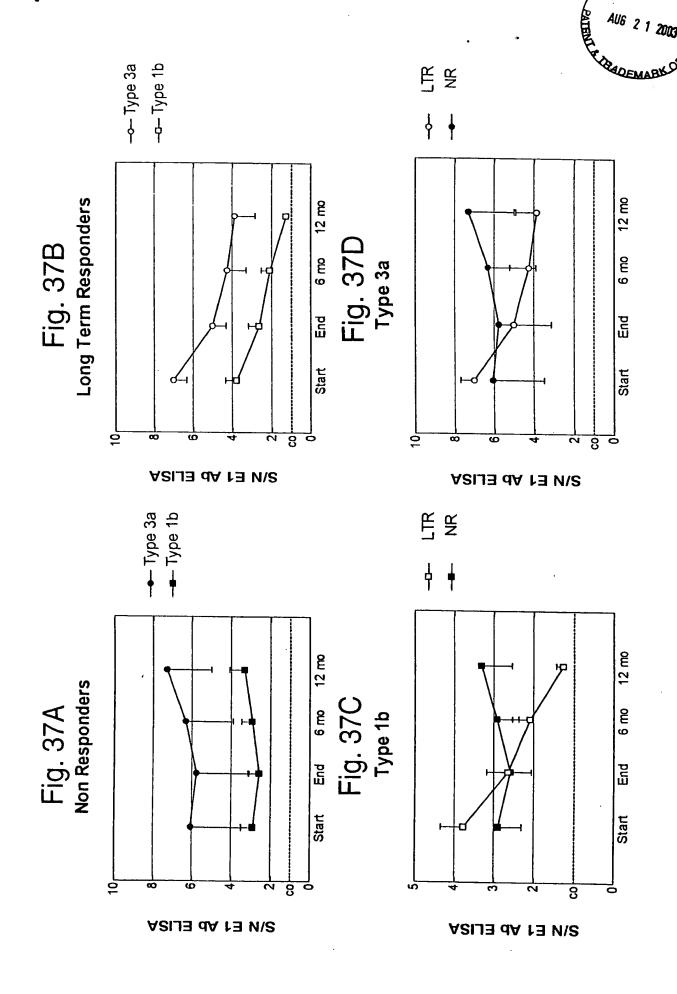
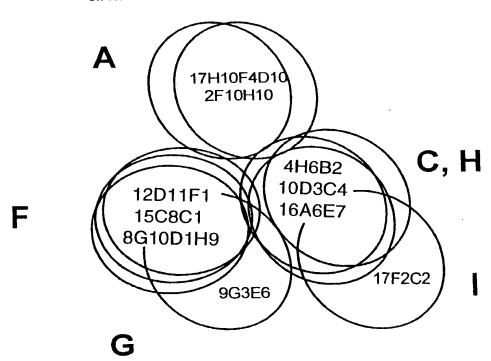




Fig. 38

Relative Map Positions of anti-E2 monoclonal antibodies





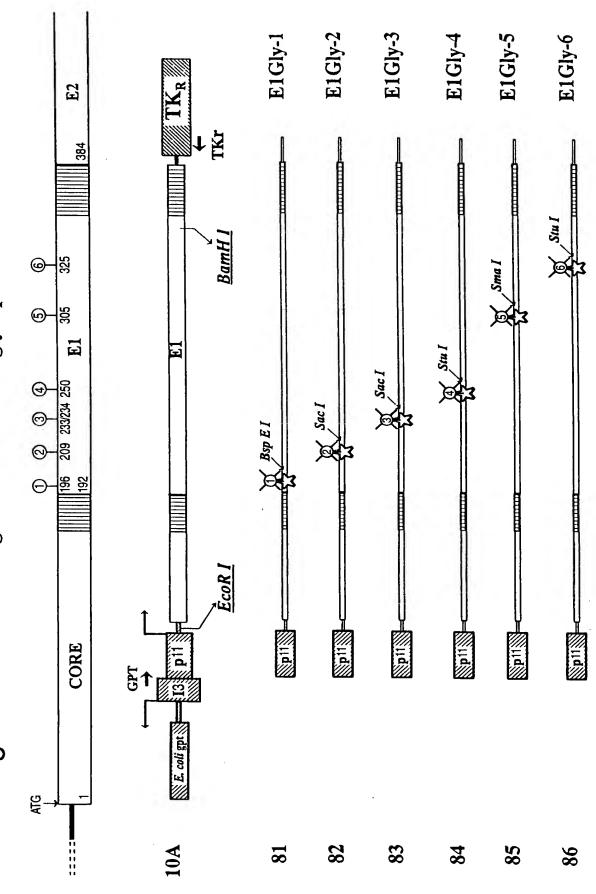
PARTIAL TREATMENT OF HCV E2\E2S ENVELOPE PROTEINS BY PNGase F

		к Ба	- 106	- 80	- 49.5	- 32.5
	E2s (vvHCV-41)	Umt				
		Umt.0				
		Umfo.0				
		UHL				
		U4r.0			1111	
		U410.0				
		-				г.,
					± 5 0 0 10 4	8 4 - 0
					Marke	
	E2 (vvHCV-64)	Մա			iv I	ę :
		Umt.0				k ?
		Umto.0			· 自然激发系	
		U41			44.14	
		Uut.0				
		U410.0			ik jak	
		-			ik Wa	. ·
		х Оа	106 -	- 08	49.5 -	32.5 -

Fig. 40

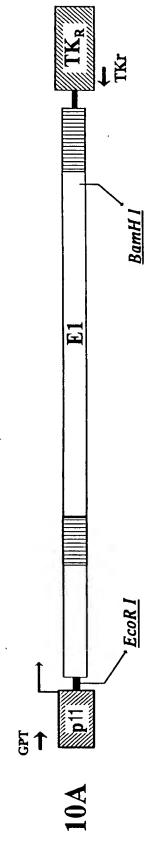


Fig. 41 In Vitro Mutagenesis of HCV E1 glycoprotein



OVR-# GLY#

Fig. 42A In Vitro Mutagenesis of HCV E1 glycoprotein



First step of PCR amplification (Gly-# and Ovr-# primers)

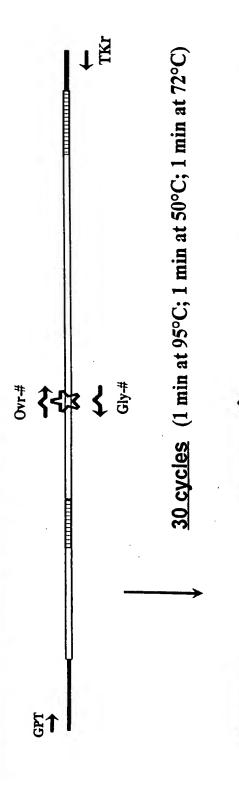
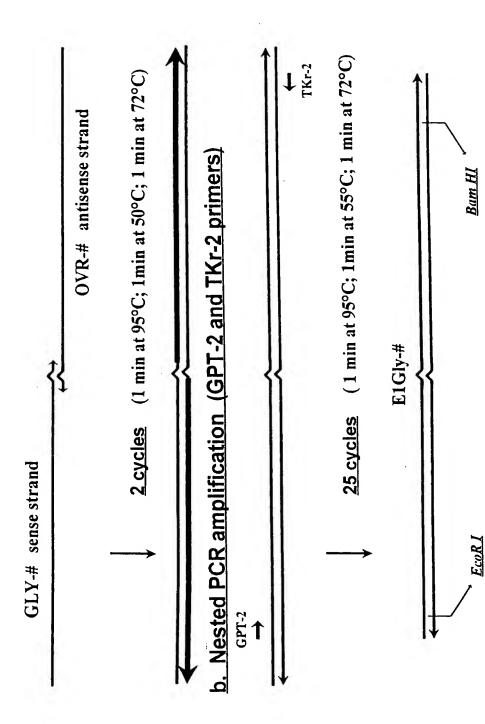






Fig. 42B



CATEMA E1Gly-2 E1Gly-3 E1Gly-5 E1Gly-4 E1Gly-6 E2 节 280 nt 340 nt 500 nt **OVR-6** BamH I OVR-5 550 nt 325 <u></u> BamH 1 630 nt **6** 770 nt GLY-5 **OVR4 OVR-3** EI OVR-2 209 233/234 250 OVR-1 710 nt O 8 5 550 nt 500 nt 420 nt Ecor I EcoR I 380 nt GPT TO THE COLUMN TO THE COLUM CORE tg**↑** 82 83 84 85 81 98

Fig. 43 In Vitro Mutagenesis of HCV E1 glycoprotein



		HeLa cells	. RK 13 cells			
		1 3 4 6 7		2 3 4 5 6 8.		
80,0			80,0	· · · · · · · · · · · · · · · · · · ·	_	80,0
49.5			— 49.5		_	49.5
32.5			_ 32.5			32.5
27.5			— 27.5		_	27.5
18.5	_		— 18.5		_	18.5

Fig. 44A



Fig.44B





Fig.45

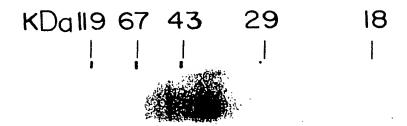


Fig.46